

## SEQUENCE LISTING

<110> DNAVEC RESEARCH INC.

<120> Methods of producing a viral vector comprising a membrane protein  
that binds to sialic acid as a component of the envelope  
using neuraminidase derived from Gram-positive bacteria

<130> D3-A0204P

<150> JP 2002-258576

<151> 2002-09-04

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1941

<212> DNA

<213> *Micromonospora viridifaciens*

<220>

<221> CDS

<222> (1).. (1941)

<223>

&lt;400&gt; 1

atg act gcg aat ccg tac ctc cgc cgc ctg ccc cgg cgc cga gcc gtc 48

Met Thr Ala Asn Pro Tyr Leu Arg Arg Leu Pro Arg Arg Arg Ala Val

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agc ttc ctg ctc gca cca gcg ctg gcg gcc gcc acg gtc gcc ggc gcg 96

Ser Phe Leu Leu Ala Pro Ala Leu Ala Ala Ala Thr Val Ala Gly Ala

20 25 30

tcc ccc gca cag gcc atc gcc ggg gca ccc gtc ccg ccc ggc ggc gag 144

Ser Pro Ala Gln Ala Ile Ala Gly Ala Pro Val Pro Pro Gly Gly Glu

35 40 45

ccg ctc tac acg gag cag gac ctc gcc gtg aac ggc agg gag ggc ttt 192

Pro Leu Tyr Thr Glu Gln Asp Leu Ala Val Asn Gly Arg Glu Gly Phe

50 55 60

ccg aac tac cgc atc cca gcg ctg acc gtc acg ccc gac ggc gac ctg 240

Pro Asn Tyr Arg Ile Pro Ala Leu Thr Val Thr Pro Asp Gly Asp Leu

65 70 75 80

ctg gcc tcg tac gac ggc cgc ccg acc ggt atc gac gcg ccc ggc ccc 288

Leu Ala Ser Tyr Asp Gly Arg Pro Thr Gly Ile Asp Ala Pro Gly Pro

85 90 95

aac tcc atc ctc caa cgc cgc agc acc gac ggc ggc cgg acg tgg ggc	336
Asn Ser Ile Leu Gln Arg Arg Ser Thr Asp Gly Gly Arg Thr Trp Gly	
100 105 110	
 gag caa cag gtc gtc agc gcc ggc cag acc acc gcg ccg atc aag ggg	384
Glu Gln Gln Val Val Ser Ala Gly Gln Thr Thr Ala Pro Ile Lys Gly	
115 120 125	
 ttc tcc gac ccc agc tac ctt gtc gac cgg gaa acc ggg acc atc ttc	432
Phe Ser Asp Pro Ser Tyr Leu Val Asp Arg Glu Thr Gly Thr Ile Phe	
130 135 140	
 aac ttc cac gtc tac tcc cag cgg cag ggc ttc gcc ggc agc cgg ccc	480
Asn Phe His Val Tyr Ser Gln Arg Gln Gly Phe Ala Gly Ser Arg Pro	
145 150 155 160	
 ggc acc gac ccg gca gac ccc aac gtg ctc cac gcc aac gtc gcg acc	528
Gly Thr Asp Pro Ala Asp Pro Asn Val Leu His Ala Asn Val Ala Thr	
165 170 175	
 tcg acc gac ggc ggt ctg acc tgg tcg cac cgg acc atc acg gcc gac	576
Ser Thr Asp Gly Gly Leu Thr Trp Ser His Arg Thr Ile Thr Ala Asp	
180 185 190	
 atc acc ccg gat ccg ggc tgg cgc agc cgc ttc gcc gcc tcc ggc gaa	624
Ile Thr Pro Asp Pro Gly Trp Arg Ser Arg Phe Ala Ala Ser Gly Glu	

195	200	205	
ggc atc cag ctc cgc tat gga ccc cac gcc ggt cga ctc atc cag cag			672
Gly Ile Gln Leu Arg Tyr Gly Pro His Ala Gly Arg Leu Ile Gln Gln			
210	215	220	
tac acg atc atc aac gct gcc ggc gcc ttc cag gcg gtg agc gtg tac			720
Tyr Thr Ile Ile Asn Ala Ala Gly Ala Phe Gln Ala Val Ser Val Tyr			
225	230	235	240
agc gac gac cac gga agg acc tgg cgc gcc ggc gaa gcc gtc ggg gtc			768
Ser Asp Asp His Gly Arg Thr Trp Arg Ala Gly Glu Ala Val Gly Val			
245	250	255	
ggc atg gac gag aac aag acc gtg gaa ctc tcc gat ggc cgg gtc ctg			816
Gly Met Asp Glu Asn Lys Thr Val Glu Leu Ser Asp Gly Arg Val Leu			
260	265	270	
ctc aac agc cgc gac tcg gcc cgc agc gga tac cgt aag gtg gcc gtc			864
Leu Asn Ser Arg Asp Ser Ala Arg Ser Gly Tyr Arg Lys Val Ala Val			
275	280	285	
tcc act gac ggc ggc cac agc tac ggc ccg gtg acc atc gac cgc gac			912
Ser Thr Asp Gly Gly His Ser Tyr Gly Pro Val Thr Ile Asp Arg Asp			
290	295	300	

ctc ccc gac ccg acg aac aac gca tcg atc atc cgg gcc ttc cct gac 960  
 Leu Pro Asp Pro Thr Asn Asn Ala Ser Ile Ile Arg Ala Phe Pro Asp  
 305 310 315 320

gcc ccg gcc ggc tcc gcg cgg gcc aag gtc ctg ctc ttc tcc aac gcc 1008  
 Ala Pro Ala Gly Ser Ala Arg Ala Lys Val Leu Leu Phe Ser Asn Ala  
 325 330 335

gcc agc cag acc tcg cgc agt cag ggc acc atc cgg atg tcc tgc gac 1056  
 Ala Ser Gln Thr Ser Arg Ser Gln Gly Thr Ile Arg Met Ser Cys Asp  
 340 345 350

gat ggc cag acc tgg ccg gtt tcg aag gtc ttc cag ccc ggc tcg atg 1104  
 Asp Gly Gln Thr Trp Pro Val Ser Lys Val Phe Gln Pro Gly Ser Met  
 355 360 365

tcg tac tcc acc ctg acc gca ctg ccc gac ggc acc tac ggg ctg ctg 1152  
 Ser Tyr Ser Thr Leu Thr Ala Leu Pro Asp Gly Thr Tyr Gly Leu Leu  
 370 375 380

tac gag ccg ggc acc ggc atc aga tac gcc aac ttc aac ctc gcc tgg 1200  
 Tyr Glu Pro Gly Thr Gly Ile Arg Tyr Ala Asn Phe Asn Leu Ala Trp  
 385 390 395 400

ctg ggc ggc atc tgc gcg ccc ttc acg att ccg gat gtg gcg ctc gag 1248  
 Leu Gly Gly Ile Cys Ala Pro Phe Thr Ile Pro Asp Val Ala Leu Glu

405	410	415	
ccg ggc cag cag gtc act gtt ccg gtg gcc gtc acg aac cag tcc ggt			1296
Pro Gly Gln Gln Val Thr Val Pro Val Ala Val Thr Asn Gln Ser Gly			
420	425	430	
atc gcg gta ccg aag ccg agc ctt cag ctc gac gca tcg ccg gac tgg			1344
Ile Ala Val Pro Lys Pro Ser Leu Gln Leu Asp Ala Ser Pro Asp Trp			
435	440	445	
cag gtt cag ggt tcc gtc gag ccc ctc atg ccc gga cgg cag gcc aag			1392
Gln Val Gln Gly Ser Val Glu Pro Leu Met Pro Gly Arg Gln Ala Lys			
450	455	460	
ggc cag gtg acc atc acg gtt ccc gcc ggc acc acc ccc ggt cgc tac			1440
Gly Gln Val Thr Ile Thr Val Pro Ala Gly Thr Thr Pro Gly Arg Tyr			
465	470	475	480
cgg gtc ggt gcg acg ctg cgc acc tcc gcg ggt aac gcg tcg acg acc			1488
Arg Val Gly Ala Thr Leu Arg Thr Ser Ala Gly Asn Ala Ser Thr Thr			
485	490	495	
ttc acg gtc acg gtt gga ctg ctc gac cag gcc cgg atg agc atc gcg			1536
Phe Thr Val Thr Val Gly Leu Leu Asp Gln Ala Arg Met Ser Ile Ala			
500	505	510	

gac gtc gac agc gag gag acc gcc cgc gaa gac ggg cgg gcg agc aac 1584

Asp Val Asp Ser Glu Glu Thr Ala Arg Glu Asp Gly Arg Ala Ser Asn

515

520

525

gtg atc gac ggc aac ccc tcg acg ttc tgg cac acc gaa tgg tcg cgt 1632

Val Ile Asp Gly Asn Pro Ser Thr Phe Trp His Thr Glu Trp Ser Arg

530

535

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gcc gat gct cct ggc tac ccg cac cgc atc agc ctc gac ctc ggt ggc 1680

Ala Asp Ala Pro Gly Tyr Pro His Arg Ile Ser Leu Asp Leu Gly Gly

545

550

555

560

acg cac acg atc agc ggc ctc cag tac acc cga cgg cag aac agc gcc 1728

Thr His Thr Ile Ser Gly Leu Gln Tyr Thr Arg Arg Gln Asn Ser Ala

565

570

575

aac gag cag gtc gcg gac tac gag atc tac acc agc ctg aac ggc acg 1776

Asn Glu Gln Val Ala Asp Tyr Glu Ile Tyr Thr Ser Leu Asn Gly Thr

580

585

590

acc tgg gat ggc ccg gtt gcc agc ggg cgc ttc acc acg tcc ctc gcg 1824

Thr Trp Asp Gly Pro Val Ala Ser Gly Arg Phe Thr Thr Ser Leu Ala

595

600

605

ccg cag cgc gcg gtc ttc ccg gcg cgg gac gcc agg tac atc cgg ttg 1872

Pro Gln Arg Ala Val Phe Pro Ala Arg Asp Ala Arg Tyr Ile Arg Leu

610                      615                      620  
 gtg gcc ctc agc gag cag acc ggg cac aag tac gcc gcg gtc gct gag      1920  
 Val Ala Leu Ser Glu Gln Thr Gly His Lys Tyr Ala Ala Val Ala Glu  
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ctg gag gtg gaa ggc cag cgc      1941  
 Leu Glu Val Glu Gly Gln Arg  
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<212> PRT

<213> *Micromonospora viridifaciens*

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Met Thr Ala Asn Pro Tyr Leu Arg Arg Leu Pro Arg Arg Arg Ala Val  
 1                      5                      10                      15

Ser Phe Leu Leu Ala Pro Ala Leu Ala Ala Ala Thr Val Ala Gly Ala  
 20                      25                      30



9/14

Ser Pro Ala Gln Ala Ile Ala Gly Ala Pro Val Pro Pro Gly Gly Glu

35

40

45

Pro Leu Tyr Thr Glu Gln Asp Leu Ala Val Asn Gly Arg Glu Gly Phe

50

55

60

Pro Asn Tyr Arg Ile Pro Ala Leu Thr Val Thr Pro Asp Gly Asp Leu

65

70

75

80

Leu Ala Ser Tyr Asp Gly Arg Pro Thr Gly Ile Asp Ala Pro Gly Pro

85

90

95

Asn Ser Ile Leu Gln Arg Arg Ser Thr Asp Gly Gly Arg Thr Trp Gly

100

105

110

Glu Gln Gln Val Val Ser Ala Gly Gln Thr Thr Ala Pro Ile Lys Gly

115

120

125

Phe Ser Asp Pro Ser Tyr Leu Val Asp Arg Glu Thr Gly Thr Ile Phe

130

135

140

Asn Phe His Val Tyr Ser Gln Arg Gln Gly Phe Ala Gly Ser Arg Pro  
145 150 155 160

Gly Thr Asp Pro Ala Asp Pro Asn Val Leu His Ala Asn Val Ala Thr  
165 170 175

Ser Thr Asp Gly Gly Leu Thr Trp Ser His Arg Thr Ile Thr Ala Asp  
180 185 190

Ile Thr Pro Asp Pro Gly Trp Arg Ser Arg Phe Ala Ala Ser Gly Glu  
195 200 205

Gly Ile Gln Leu Arg Tyr Gly Pro His Ala Gly Arg Leu Ile Gln Gln  
210 215 220

Tyr Thr Ile Ile Asn Ala Ala Gly Ala Phe Gln Ala Val Ser Val Tyr  
225 230 235 240

Ser Asp Asp His Gly Arg Thr Trp Arg Ala Gly Glu Ala Val Gly Val

245

250

255

Gly Met Asp Glu Asn Lys Thr Val Glu Leu Ser Asp Gly Arg Val Leu

260

265

270

Leu Asn Ser Arg Asp Ser Ala Arg Ser Gly Tyr Arg Lys Val Ala Val

275

280

285

Ser Thr Asp Gly Gly His Ser Tyr Gly Pro Val Thr Ile Asp Arg Asp

290

295

300

Leu Pro Asp Pro Thr Asn Asn Ala Ser Ile Ile Arg Ala Phe Pro Asp

305

310

315

320

Ala Pro Ala Gly Ser Ala Arg Ala Lys Val Leu Leu Phe Ser Asn Ala

325

330

335

Ala Ser Gln Thr Ser Arg Ser Gln Gly Thr Ile Arg Met Ser Cys Asp

340

345

350

Asp Gly Gln Thr Trp Pro Val Ser Lys Val Phe Gln Pro Gly Ser Met

355

360

365

Ser Tyr Ser Thr Leu Thr Ala Leu Pro Asp Gly Thr Tyr Gly Leu Leu

370

375

380

Tyr Glu Pro Gly Thr Gly Ile Arg Tyr Ala Asn Phe Asn Leu Ala Trp

385

390

395

400

Leu Gly Gly Ile Cys Ala Pro Phe Thr Ile Pro Asp Val Ala Leu Glu

405

410

415

Pro Gly Gln Gln Val Thr Val Pro Val Ala Val Thr Asn Gln Ser Gly

420

425

430

Ile Ala Val Pro Lys Pro Ser Leu Gln Leu Asp Ala Ser Pro Asp Trp

435

440

445

Gln Val Gln Gly Ser Val Glu Pro Leu Met Pro Gly Arg Gln Ala Lys

450

455

460

Gly Gln Val Thr Ile Thr Val Pro Ala Gly Thr Thr Pro Gly Arg Tyr

465

470

475

480

Arg Val Gly Ala Thr Leu Arg Thr Ser Ala Gly Asn Ala Ser Thr Thr

485

490

495

Phe Thr Val Thr Val Gly Leu Leu Asp Gln Ala Arg Met Ser Ile Ala

500

505

510

Asp Val Asp Ser Glu Glu Thr Ala Arg Glu Asp Gly Arg Ala Ser Asn

515

520

525

Val Ile Asp Gly Asn Pro Ser Thr Phe Trp His Thr Glu Trp Ser Arg

530

535

540

Ala Asp Ala Pro Gly Tyr Pro His Arg Ile Ser Leu Asp Leu Gly Gly

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555

560

Thr His Thr Ile Ser Gly Leu Gln Tyr Thr Arg Arg Gln Asn Ser Ala

565

570

575

Asn Glu Gln Val Ala Asp Tyr Glu Ile Tyr Thr Ser Leu Asn Gly Thr

580

585

590

Thr Trp Asp Gly Pro Val Ala Ser Gly Arg Phe Thr Thr Ser Leu Ala

595

600

605

Pro Gln Arg Ala Val Phe Pro Ala Arg Asp Ala Arg Tyr Ile Arg Leu

610

615

620

Val Ala Leu Ser Glu Gln Thr Gly His Lys Tyr Ala Ala Val Ala Glu

625

630

635

640

Leu Glu Val Glu Gly Gln Arg

645